Package ‘clickstream’

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Type Package
Title Analyzes Clickstreams Based on Markov Chains
Version 1.2.1
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Author Michael Scholz
Maintainer Michael Scholz <michael.scholz@uni-passau.de>
Description A set of tools to read, analyze and write lists of click sequences
on websites (i.e., clickstream). A click can be represented by a number,
character or string. Clickstreams can be modeled as zero- (only computes
occurrence probabilities), first- or higher-order Markov chains.
License GPL-2
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Description

This package allows modeling clickstreams with Markov chains. It supports to model clickstreams as zero-order, first-order or higher-order Markov chains.

Details

Package: clickstream
Type: Package
Version: 1.2.1
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License: GPL-2
Depends: R (>= 3.0), methods

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

References

Examples

# fitting a simple Markov chain and predicting the next click
clickstreams <- c("User1, h, c, c, p, c, h, c, p, p, c, p, p, o",
                   "User2, i, c, i, c, c, c, d",
                   "User3, h, i, c, i, c, p, c, p, c, c, i, d",
                   "User4, c, c, p, c, d",
                   "User5, h, c, c, p, p, c, p, p, p, i, p, o",
                   "User6, i, h, c, c, p, p, c, p, c, d")

csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
startPattern <- new("Pattern", sequence = c("h", "c"))
predict(mc, startPattern)
plot(mc)

absorbingStates

Description

Returns All Absorbing States

Usage

absorbingStates(object)

Arguments

  object An instance of the MarkovChain-class

Methods

  list("signature(object = \"MarkovChain\")") Returns the names of all states that never have a
successor in a clickstream (i.e. that are absorbing).

Author(s)

  Michael Scholz <michael.scholz@uni-passau.de>
Coerces a Clickstream Object to a ClickClust Object

Description

Coerces a clickstream object to a ClickClust object.

Usage

as.ClickClust(clickstreamList)

Arguments

clickstreamList

A list of clickstreams.

Value

A list consisting of a dataset X and a vector of initial states y

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

frequencies

Examples

clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                  "User2,i,c,i,c,c,d",
                  "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,c,p,c,p,p,i,p,o",
                  "User6,i,h,c,c,p,c,p,c,c,d")
csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
X <- as.ClickClust(cls)
as.transactions

Coerces a Clickstream Object to a Transactions Object

Description

Coerces a Clickstream object to a transactions object.

Usage

as.transactions(clickstreamList)

Arguments

clickstreamList  
A list of clickstreams.

Value

An instance of the class transactions

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

frequencies

Examples

```
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",  
  "User2,i,c,c,c,c,d",  
  "User3,h,i,c,i,c,p,c,c,p,i,d",  
  "User4,c,c,p,c,d",  
  "User5,h,c,c,p,c,p,i,p,o",  
  "User6,i,h,c,c,p,p,c,c,d")

csf <- tempfile()  
writelines(clickstreams, csf)  
cls <- readClickstreams(csf, header = TRUE)  
trans <- as.transactions(cls)
```
clusterClickstreams  Performs K-Means Clustering on a List of Clickstreams

Description

Performs k-means clustering on a list of clickstreams. For each clickstream a transition matrix of a given order is computed. These transition matrices are used as input for performing k-means clustering.

Usage

clusterClickstreams(clickstreamList, order = 0, centers, ...)

Arguments

clickstreamList  
A list of clickstreams for which the cluster analysis is performed.

order  
The order of the transition matrices used as input for clustering (default is 0; 0 and 1 are possible).

centers  
The number of clusters.

...  
Additional parameters for k-means clustering (see kmeans).

Value

This method returns a ClickstreamClusters object (S3-class). It is a list with the following components:

clusters  
The resulting list of Clickstreams objects.

centers  
A matrix of cluster centres.

states  
Vector of states

totss  
The total sum of squares.

withinss  
Vector of within-cluster sum of squares, one component per cluster.

tot.withinss  
Total within-cluster sum of squares, i.e., \( \text{sum(withinss)} \).

betweenss  
The between-cluster sum of squares, i.e., \( \text{totss} - \text{tot.withinss} \).

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

print.ClickstreamClusters, summary.ClickstreamClusters
Examples

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o", 
    "User2,i,c,i,c,c,c,d", 
    "User3,h,i,c,i,c,p,c,p,c,i,d", 
    "User4,c,c,p,c,d", 
    "User5,h,c,c,p,c,p,p,i,p,o", 
    "User6,i,h,c,c,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
clusters <- clusterClickstreams(cls, order = 0, centers = 2)
print(clusters)
```

fitMarkovChain

Fits a List of Clickstreams to a Markov Chain

Description

This function fits a list of clickstreams to a Markov chain. Zero-order, first-order as well as higher-order Markov chains are supported. For estimating higher-order Markov chains this function solves the following linear or quadratic programming problem:

\[
\min \left| \sum_{i=1}^{k} X - \lambda_i Q_i X \right| \\
\text{s.t.} \\
\sum_{i=1}^{k} \lambda_i = 1 \\
\lambda_i \geq 0
\]

The distribution of states is given as \( X \). \( \lambda_i \) is the lag parameter for lag \( i \) and \( Q_i \) the transition matrix.

Usage

```r
fitMarkovChain(clickstreamList, order = 1, verbose = TRUE, 
control = list())
```

Arguments

- `clickstreamList`  
  A list of clickstreams for which a Markov chain is fitted.

- `order`  
  (Optional) The order of the Markov chain that is fitted from the clickstreams. Per default, Markov chains with order=1 are fitted. It is also possible to fit zero-order Markov chains (order=0) and higher-order Markov chains.
verbose  (Optional) An optimal logical variable to indicate whether warnings and infos should be printed.

control  (Optional) The control list of optimization parameters. Parameter optimizer specifies the type of solver used to solve the given optimization problem. Possible values are "linear" (default) and "quadratic". Parameter use.lpSolve determines whether lpSolve or linprog is used as linear solver.

Details
For solving the quadratic programming problem of higher-order Markov chains, an augmented Lagrange multiplier method from the package Rsolnp is used.

Value
Returns a MarkovChain object.

Note
At least half of the clickstreams need to consist of as many clicks as the order of the Markov chain that should be fitted.

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

References

See Also
MarkovChain, Rsolnp

Examples

```r
# fitting a simple Markov chain
clickstreams <- c("User1,h,c,p,c,h,c,p,p,p,p,o",
                   "User2,i,c,i,c,c,c,d",
                   "User3,h,i,c,i,c,p,c,p,c,c,i,d",
                   "User4,c,c,p,c,d",
                   "User5,h,c,c,p,p,p,p,p,i,p,o",
                   "User6,i,h,c,c,p,p,p,c,c,d")
csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
show(mc)
```
frequencies

Generates a Data Frame of State Frequencies for All Clickstreams in a List of Clickstreams

**Description**

Generates a data frame of state frequencies for all clickstreams in a list of clickstreams.

**Usage**

```r
frequencies(clickstreamList)
```

**Arguments**

- `clickstreamList`
  
  A list of clickstreams.

**Value**

A data frame containing state frequencies for each clickstream.

**Author(s)**

Michael Scholz <michael.scholz@uni-passau.de>

**See Also**

transactions

**Examples**

```r
# Example clickstreams
clickstreams <- c("User1,h,c,p,c,h,c,p,p,c,p,p,o", 
                  "User2,i,c,i,c,c,c,d", 
                  "User3,h,i,c,i,c,p,c,p,c,c,i,d", 
                  "User4,c,c,p,c,d", 
                  "User5,h,c,c,p,p,c,p,p,i,p,o", 
                  "User6,i,h,c,c,p,p,c,c,d")

# Write to temporary file
csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
frequencyDF <- frequencies(cls)
```
hmPlot

Plots a Heatmap

Description

Plots a Heatmap

Usage

hmPlot(object, order = 1, absorptionProbability = FALSE, title = NA, lowColor = "yellow", highColor = "red", flip = FALSE)

Arguments

object The MarkovChain for which a heatmap is plotted.
order Order of the transition matrix that should be plotted. Default is 1.
absorptionProbability Should the heatmap show absorption probabilities? Default is FALSE.
title Title of the heatmap.
lowColor Color for the lowest transition probability of 0. Default is "yellow".
highColor Color for the highest transition probability of 1. Default is "red".
flip Flip to horizontal plot. Default is FALSE.

Methods

list("signature(object = "MarkovChain")") 
Plots a heatmap for a specified transition matrix or the absorption probability matrix of a given MarkovChain object.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

fitMarkovChain

Examples

# fitting a simple Markov chain and predicting the next click
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o", "User2,i,c,i,c,c,c,d", "User3,h,i,c,i,c,p,c,c,p,c,i,d", "User4,c,c,p,c,d", "User5,h,c,c,p,p,c,p,p,p,i,o", "User6,i,h,c,c,p,p,c,p,c,d")

csf <- tempfile()
```r
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
hmPlot(mc)
```

---

### MarkovChain-class

**Class** "MarkovChain"

#### Description

Class "MarkovChain"

#### Objects from the Class

Objects can be created by calls of the form `new("MarkovChain", ...)`. This S4 class describes MarkovChain objects.

#### Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

#### See Also

- `fitMarkovChain`

#### Examples

```r
# show MarkovChain definition
showClass("MarkovChain")

# fit a simple Markov chain from a list of click streams
clickstreams <- c("User1,h,c,c,p,h,c,p,p,c,p,p,o",
                  "User2,i,c,i,c,c,d",
                  "User3,h,i,c,i,c,p,c,c,p,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,c,p,c,p,p,i,p,o",
                  "User6,i,h,c,c,p,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
show(mc)
```
Pattern-class  

Class "Pattern"

Description

This S4 class describes a click pattern consisting of a sequence of clicks and a probability of occurrence.

Objects from the Class

Objects can be created by calls of the form `new("Pattern", sequence, probability, ...)`. This S4 class describes a click pattern consisting of a sequence of clicks and a probability of occurrence.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

randomClicks

Examples

```r
# show Pattern definition
showClass("Pattern")

# create simple Pattern objects
pattern1 <- new("Pattern", sequence = c("h", "c", "p"))
pattern2 <- new("Pattern", sequence = c("c", "p", "p"), probability = 0.2)
pattern3 <- new("Pattern", sequence = c("h", "p", "p"), probability = 0.35,
absorbingProbabilities = data.frame(d = 0.6, o = 0.4))
```

predict,MarkovChain-method

*Predicts the Next Click(s) of a User*

Description

Predicts the Next Click(s) of a User

Usage

```r
## S4 method for signature 'MarkovChain'
predict(object, startPattern, dist = 1,
        ties = "random")
```
predict.MarkovChain-method

Arguments

- object: The MarkovChain used for predicting the next click(s).
- startPattern: Starting clicks of a user as Pattern object. A Pattern with an empty sequence is also possible.
- dist: (Optional) The number of clicks that should be predicted (default is 1).
- ties: (Optional) The strategy for handling ties in predicting the next click. Possible strategies are `random` (default) and `first`.

Methods

- `list("signature(object = "MarkovChain")")`: This method predicts the next click(s) of a user. The first clicks of a user are given as Pattern object. The next click(s) are predicted based on the transition probabilities in the MarkovChain object. The probability distribution of the next click \( n \) is estimated as follows:

\[
X^{(n)} = B \sum_{i=1}^{k} \lambda_i Q_i X^{(n-i)}
\]

The distribution of states at time \( n \) is given as \( X^n \). The transition matrix for lag \( i \) is given as \( Q_i \), \( \lambda_i \) specifies the lag parameter and \( B \) the absorbing probability matrix.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

- `fitMarkovChain`

Examples

```r
# fitting a simple Markov chain and predicting the next click
clickstreams <- c("User1,h,c,p,c,h,c,p,p,p,o",
                  "User2,i,c,i,c,c,d",
                  "User3,h,i,c,i,c,p,c,p,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,p,c,p,p,p,i,p,o",
                  "User6,i,h,c,c,p,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
startPattern <- new("Pattern", sequence = c("h", "c"))
predict(mc, startPattern)
# # predict with predefined absorbing probabilities
# startPattern <- new("Pattern", sequence = c("h", "c"),
# absorbingProbabilities = data.frame(d = 0.2, o = 0.8))
```
predict(object, pattern, ...)
clusters <- clusterClickstreams(cls, order = 0, centers = 2)
pattern <- new("Pattern", sequence = c("h", "c"))
predict(clusters, pattern)

print.ClickstreamClusters

Prints a ClickstreamClusters Object

Description
Prints a ClickstreamClusters object. A ClickstreamClusters object represents the result of a cluster analysis on a list of clickstreams (see clusterClickstreams).

Usage
## S3 method for class 'ClickstreamClusters'
print(x, ...)

Arguments
x 
A ClickstreamClusters object (see clusterClickstreams).

... 
Ignored parameters.

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

See Also
clusterClickstreams, summary.ClickstreamClusters

Examples

clickstreams <- c("User1,h,c,p,c,h,c,p,p,c,p,p,o",
                  "User2,i,c,i,c,c,c,d",
                  "User3,h,i,c,i,p,c,c,p,c,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,c,p,p,c,p,p,i,p,o",
                  "User6,i,h,c,c,p,p,c,c,d")
csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
clusters <- clusterClickstreams(cls, order = 0, centers = 2)
print(clusters)
prints a Clickstreams object

## Usage

```r
## S3 method for class 'Clickstreams'
print(x, ...)
```

## Arguments

- `x`: A list of clickstreams.
- `...`: Ignored parameters.

## Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

## See Also

- `readClickstreams`
- `randomClickstreams`

## Examples

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o","User2,i,c,c,c,c,d","User3,h,i,c,c,p,c,c,c,c,i,d","User4,c,c,p,c,d","User5,h,c,c,p,p,c,p,p,i,p,o","User6,i,h,c,c,p,c,p,c,d")
csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
print(cls)
```
print.MarkovChainSummary

Prints the Summary of a MarkovChain Object

Description

Prints the summary of a MarkovChain object.

Usage

```r
## S3 method for class 'MarkovChainSummary'
print(x, ...)
```

Arguments

- `x` A MarkovChainSummary object generated with the function `summary`
- `...` Ignored parameters.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

`summary`

Examples

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                   "User2,i,c,i,c,c,c,d",
                   "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                   "User4,c,c,p,c,d",
                   "User5,h,c,c,p,p,p,i,p,o",
                   "User6,i,h,c,c,p,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
print(summary(mc))
```
randomClicks  Generates a Sequence of Clicks

Description
Generates a Sequence of Clicks

Usage
randomClicks(object, startPattern, dist)

Arguments
- object: The MarkovChain used for generating the next click(s)
- startPattern: Pattern containing the first clicks of a user. A Pattern object with an empty sequence is also possible.
- dist: (Optional) The number of clicks that should be generated (default is 1).

Methods
- list("signature(object = \"MarkovChain\")")  Generates a sequence of clicks by randomly walking through the transition graph of a given MarkovChain object.

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

See Also
- fitMarkovChain

Examples
```r
# fitting a simple Markov chain and predicting the next click
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o", "User2,i,c,i,c,c,d", "User3,h,i,c,i,c,p,c,c,p,c,i,d", "User4,c,c,p,c,d", "User5,h,c,c,p,c,p,p,i,p,o", "User6,i,h,c,c,p,c,p,c,d")

csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
startPattern <- new("Pattern", sequence = c("h", "c"))
predict(mc, startPattern)
```
randomClickstreams  

Generates a List of Clickstreams

Description
Generates a list of clickstreams by randomly walking through a given transition matrix.

Usage
randomClickstreams(states, startProbabilities, transitionMatrix, meanLength, n = 100)

Arguments
- states: Names of all possible states.
- startProbabilities: Start probabilities for all states.
- transitionMatrix: Matrix of transition probabilities.
- meanLength: Average length of the click streams.
- n: Number of click streams to be generated.

Value
Returns a list of clickstreams.

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

See Also
- fitMarkovChain
- readClickstreams
- print.Clickstreams

Examples

# generate a simple list of click streams
states <- c("a", "b", "c")
startProbabilities <- c(0.2, 0.5, 0.3)
transitionMatrix <- matrix(c(0, 0.4, 0.6, 0.3, 0.1, 0.6, 0.2, 0.8, 0), nrow = 3)
cls <- randomClickstreams(states, startProbabilities, transitionMatrix, meanLength = 5, n = 10)
print(cls)
readClickstreams  

Reads a List of Clickstreams from File

Description

Reads a list of clickstream from a csv-file.

Usage

readClickstreams(file, sep = ",", header = FALSE)

Arguments

file
The name of the file which the clickstreams are to be read from. Each line of the file appears as one click stream. If it does not contain an absolute path, the file name is relative to the current working directory, getwd.

sep
The character separating clicks (default is ",").

header
A logical flag indicating whether the first entry of each line in the file is the name of the clickstream user.

Value

A list of clickstreams. Each element is a vector of characters representing the clicks. The name of each list element is either the header of a clickstream file or a unique number.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

print.Clickstreams, randomClickstreams

Examples

clickstreams <- c("User1,h,c,c,p,h,c,p,p,c,p,p,o","User2,i,c,i,c,c,d","User3,h,i,c,i,c,p,c,p,c,c,i,d","User4,c,c,p,c,d","User5,h,c,c,p,p,p,p,i,p,o","User6,i,h,c,c,p,p,c,c,d")
csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
print(cls)
show.Pattern-method  Shows a Pattern Object

Description
Shows a Pattern Object

Usage
```r
## S4 method for signature 'Pattern'
show(object)
```

Arguments
- `object` An instance of the Pattern-class

Methods
```r
list("signature(object = "MarkovChain")")
```

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

states  Returns All States

Description
Returns All States

Usage
```r
states(object)
```

Arguments
- `object` An instance of the MarkovChain-class

Methods
```r
list("signature(object = "MarkovChain")")
```

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>
summary,MarkovChain-method

Prints the Summary of a MarkovChain Object

Description

Prints the Summary of a MarkovChain Object

Usage

## S4 method for signature 'MarkovChain'
summary(object)

Arguments

object
An instance of the MarkovChain-class

Value

Returns a MarkovChainSummary object.

list("desc")  A short description of the MarkovChain object.
list("observations")
   The number of observations from which the MarkovChain has been fitted.
list("k")  The number of estimation parameters.
list("logLikelihood")
   The maximal log-likelihood of the MarkovChain estimation.
list("aic")  Akaike's Information Criterion for the MarkovChain object
list("bic")  Bayesian Information Criterion for the MarkovChain object

Methods

list("signature(object = \"MarkovChain\")") Generates a summary for a given MarkovChain object

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>
summary.ClickstreamClusters
Prints a Summary of a ClickstreamCluster Object

Description
Prints a summary of a ClickstreamCluster object. A ClickstreamClusters object represents the result of a cluster analysis on a list of clickstreams (see clusterclickstreams).

Usage
```
## S3 method for class 'ClickstreamClusters'
summary(object, ...)  
```

Arguments
- **object**: A ClickstreamClusters object returned by clusterclickstreams.
- **...**: Ignored parameters.

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

See Also
- clusterclickstreams, print.ClickstreamClusters

Examples
```
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                   "User2,i,c,i,c,c,c,d",
                   "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                   "User4,c,c,p,c,d",
                   "User5,h,c,c,p,c,p,p,i,p,o",
                   "User6,i,h,c,c,p,c,p,c,c,d")
csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
clusters <- clusterclickstreams(cls, order = 0, centers = 2)
summary(clusters)
```
summary.Clickstreams  Prints a Summary of a Clickstreams Object

Description

Prints a summary of a Clickstreams object.

Usage

## S3 method for class 'Clickstreams'
summary(object, ...)

Arguments

object  A Clickstreams object (see readClickstreams).
...  Ignored parameters.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

readClickstreams, randomClickstreams

Examples

clickstreams <- c("User1,h,c,p,c,h,c,p,p,c,p,p,o",  
  "User2,h,c,i,c,c,c,h,d",  
  "User3,h,i,c,i,c,p,c,p,c,c,i,d",  
  "User4,c,c,p,c,d",  
  "User5,h,c,c,p,c,p,p,i,p,o",  
  "User6,h,c,c,p,c,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
summary(cls)
transientStates

Returns All Transient States

Description

Returns All Transient States

Usage

transientStates(object)

Arguments

object An instance of the MarkovChain-class

Methods

list("signature(object = \"MarkovChain\")") Returns the names of all states that have a non-zero probability that a user will never return to them (i.e. that are transient).

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

writeClickstreams

Writes a List of Clickstreams to File

Description

Writes a list of clickstream to a csv-file.

Usage

writeClickstreams(clickstreamList, file, header = TRUE, sep = ",",",
quote = TRUE)

Arguments

clickstreamList The list of clickstreams to be written.
file The name of the file which the clickstreams are written to.
header A logical flag indicating whether the name of each clickstream element should be used as first element.
sep The character used to separate clicks (default is ",").
quote A logical flag indicating whether each element of a clickstream will be surrounded by double quotes (default is TRUE).
**Author(s)**

Michael Scholz <michael.scholz@uni-passau.de>

**See Also**

`readClickstreams`, `clusterClickstreams`

**Examples**

```r
# read clickstreams
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                  "User2,i,c,i,c,c,c,d",
                  "User3,h,i,c,i,c,p,c,p,c,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,c,p,c,p,p,i,p,o",
                  "User6,i,h,c,c,p,c,p,c,d")

# write clickstreams to a temporary file
csf <- tempfile()
writeLines(clickstreams, csf)

csf <- readClickstreams(csf, header = TRUE)
clusters <- clusterClickstreams(csf, order = 0, centers = 2)
writeClickstreams(clusters, file = "clickstreams.csv", header = TRUE, sep = ",")
```
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